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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/907,263

DATE: 08/13/2001

TIME: 13:28:55

Input Set : N:\Crf3\RULE60\09907263.txt

Output Set: N:\CRF3\08132001\I907263.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Bendele, Alison M.

7 Sennello, Regina M.

8 Edwards, Carl K.

10 (ii) TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING

11 PROTEIN FOR TREATING TNF-MEDIATED DISEASES

13 (iii) NUMBER OF SEQUENCES: 4

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Amgen Inc.

17 (B) STREET: 1840 DeHavilland Drive

18 (C) CITY: Thousand Oaks

19 (D) STATE: CA

20 (E) COUNTRY: US

21 (F) ZIP: 91320-1789

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/907,263

C--> 31 (B) FILING DATE: 17-Jul-2001

32 (C) CLASSIFICATION:

46 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 09/326,394

36 (B) FILING DATE: 1999-06-04

39 (A) APPLICATION NUMBER: US 60/036,355

40 (B) FILING DATE: 23-JAN-1997

43 (A) APPLICATION NUMBER: US 60/039,315

44 (B) FILING DATE: 07-FEB-1997

47 (A) APPLICATION NUMBER: US 60/052,023

48 (B) FILING DATE: 09-JUL-1997

50 (viii) ATTORNEY/AGENT INFORMATION:

51 (A) NAME: Zindrick, Thomas K.

52 (B) REGISTRATION NUMBER: 32,185

53 (C) REFERENCE/DOCKET NUMBER: A-430D

56 (2) INFORMATION FOR SEQ ID NO: 1:

58 (i) SEQUENCE CHARACTERISTICS:

59 (A) LENGTH: 483 base pairs

60 (B) TYPE: nucleic acid

61 (C) STRANDEDNESS: unknown

62 (D) TOPOLOGY: unknown

64 (ii) MOLECULE TYPE: cDNA

67 (ix) FEATURE:

68 (A) NAME/KEY: CDS

69 (B) LOCATION: 1..483

ENTERED

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72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG      48
75 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
76 1      5      10      15
78 ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT      96
79 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
80      20      25      30
82 CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC      144
83 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
84      35      40      45
86 TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA      192
87 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
88      50      55      60
90 TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC      240
91 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
92 65      70      75      80
94 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG      288
95 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
96      85      90      95
98 AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG      336
99 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
100      100      105      110
102 ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC      384
103 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
104      115      120      125
106 CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC      432
107 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
108      130      135      140
110 TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG      480
111 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
112 145      150      155      160
114 AAT      483
115 Asn
119 (2) INFORMATION FOR SEQ ID NO: 2:
121      (i) SEQUENCE CHARACTERISTICS:
122          (A) LENGTH: 161 amino acids
123          (B) TYPE: amino acid
124          (D) TOPOLOGY: linear
126      (ii) MOLECULE TYPE: protein
128      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
130 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
131 1      5      10      15
133 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
134      20      25      30
136 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
137      35      40      45
139 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
140      50      55      60
142 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp

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143 65          70          75          80
145 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
146          85          90          95
148 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
149          100          105          110
151 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
152          115          120          125
154 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
155          130          135          140
157 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
158 145          150          155          160
160 Asn
163 (2) INFORMATION FOR SEQ ID NO: 3:
165 (i) SEQUENCE CHARACTERISTICS:
166 (A) LENGTH: 705 base pairs
167 (B) TYPE: nucleic acid
168 (C) STRANDEDNESS: unknown
169 (D) TOPOLOGY: unknown
171 (ii) MOLECULE TYPE: cDNA
174 (ix) FEATURE:
175 (A) NAME/KEY: CDS
176 (B) LOCATION: 1..705
179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
181 TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC 48
182 Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
183 1 5 10 15
185 ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC 96
186 Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
187 20 25 30
189 AGC AAG TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC 144
190 Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
191 35 40 45
193 TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC 192
194 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
195 50 55 60
197 TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT 240
198 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
199 65 70 75 80
201 GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC 288
202 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
203 85 90 95
205 ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC 336
206 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
207 100 105 110
209 CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC 384
210 Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
211 115 120 125
213 AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG 432
214 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro

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```

215      130      135      140
217 GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC      480
218 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
219 145      150      155      160
221 CAG ATC TGT AAC GTG GCC ATC CCT GGG AAT GCA AGC AGG GAT GCA      528
222 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
223      165      170      175
225 GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA GGG GCA GTA      576
226 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
227      180      185      190
229 CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG CAG CCA ACT      624
230 His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
231      195      200      205
233 CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC CCA ATG GGC      672
234 Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
235      210      215      220
237 CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC      705
238 Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
239 225      230      235
242 (2) INFORMATION FOR SEQ ID NO: 4:
244 (i) SEQUENCE CHARACTERISTICS:
245 (A) LENGTH: 235 amino acids
246 (B) TYPE: amino acid
247 (D) TOPOLOGY: linear
249 (ii) MOLECULE TYPE: protein
251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
253 Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
254 1      5      10      15
256 Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
257      20      25      30
259 Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
260      35      40      45
262 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
263      50      55      60
265 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
266 65      70      75      80
268 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
269      85      90      95
271 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
272      100      105      110
274 Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
275      115      120      125
277 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
278      130      135      140
280 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
281 145      150      155      160
283 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
284      165      170      175
286 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val

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287				180				185					190			
289	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr
290				195				200					205			
292	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly
293		210					215					220				
295	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp					
296	225					230					235					

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09907263.txt

Output Set: N:\CRF3\08132001\I907263.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]